

54

46180 434680
-0540

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2002..3081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCTAGCCACC AGTGACGATG CCTTGAATTT GGCCATTCTG ACCCAGGCCC GTATTCTGAA	60
TCCTCCGCGCATT CGCATTGTTA ATCGTTTGTG CAACCATGCC CTGGGTAAAC GTTTAGACAC	120
CACCTTGCCA GACCACGTTA GTTTGAGTGT TTCCGCCCTG GCGGCCCCGA TTTTTCCTT	180
TCGCGGCTTTG GGCAATCAGG CGATCGGGCA ATTGCGTTTG TTTGACCAGA CTTGGCCCAT	240
TCAGGAAATT GTCATTCACC AAGACCATCC CTGGCTCAAT TTACCCCTGG CGGATTTATG	300
GGATGATCCG AGCCGAATGT TGATCTATTA CCTACCGGCC CACAGTGAAA CGGATTTAGT	360
AGGCGCAGTG GTGAATAATT TAACGTTGCA ATCTGGGGAC CATTTAATAG TGGGACAAAA	420
ACCCCAACCC AAGACCAAAC GGCGATCGCC TTGGCGCAA TTTTCCAAAC TGATTACCAA	480
TCCTGCGGGAG TATCAGCGGT ATGTCCAACA GGTGATATGG GTGGTGTTGT TTTTATTGTT	540
GATGATTTTT CTGGCCACCT TCATCTACGT TTCCATTGAT CAACATATTG CCCCAGTGGA	600
CGCGTTGTAT TTTTCCGTGG GCATGATTAC CGGGGCCGGT GGCAAGGAAG AGGTGGCCGA	660
AAAGTCCCCC GATATCATCA AAGTATTCAC AGTGGTGATG ATGATCGCCG GGGCGGGGGT	720
GATTGGTATT TGTTATGCCC TACTGAATGA TTTTCATCCTT GGCAGTCGCT TTAGTCAGTT	780
TTTGGATGCG GCCAAGTTAC CCGATCGCCA TCACATCATC ATTTGTGGGC TGGGGGGAGT	840
GAGCATGGCC ATTATTGAAG AGTTAATTCA CCAGGGCCAT GAAATTGTGG TAATCGAAAA	900

GGATACAGAT AATCGTTTCT TGCATACGGC CCGCTCCCTG GGGGTGCCCCG TAATTGTGGA	960
GGATGCCCCG CTAGAAAGAA CGTTGGCCTG CGCCAATATC AACCGAGCCG AAGCCATTGT	1020
GGTGGCCACC AGCGACGACA CCGTTAACTT GGAAATTGGC CTAAGTGCCA AGGCGATCGC	1080
CCCTAGCCTG CCAGTGGTGT TGC GTTGCCA GGATGCCCAG TTTAGCCTGT CCCTGCAGGA	1140
AGTATTTGAA TTTGAAACGG TGCTTTGTCC GCGGGAATTG GCCACCTATT CCTTTGCGGC	1200
GGCGGCCCTG GGGGGCAAAA TTTTGCGCAA CGGCATGACC GATGATTTGC TGTGGGTAGC	1260
CCTAGCCACC TTAATCACTC CTAACCATCC CTTTGCCGAC CAATTGGTTA AAATTGCAGC	1320
CCAAAAGTCT GATTTCTGTTT CCCTCTATCT AGAACGGGGT GGCAAAACCA TCCATAGCTG	1380
GGGAATTATTG GGTACCCATC TCGACTCTGG AGACGTGTTG TATTTAACCA TGCCCCGCCAC	1440
GGCCCTAGAG CAACTTTGGC GATCGCCCCG TGCCACTGCT GATCCTCTGG ACTCTTTTTT	1500
GGTTTAGCAT GGGGGGATGG AACTCTTGAC TCGGCCCAAT GGTGATCAAG AAAGAACGCT	1560
TGTGCTATGT TTAGTATTTT TAAGTTAACC AACAGCAGAG GATAACTTCC AAAAGAAATT	1620
AAGCTCAAAA AGTAGCAAAA TAAGTTTAAT TCATAACTGA GTTTTACTGC TAAACAGCGG	1680
TGCAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT TATATTGTGA CCATGGTTCC	1740
CAGGCATCTG CTCTAGGGAG TTTTTCGCT GCCTTTAGAG AGTATTTTCT CCAAGTCGGC	1800
TAACTCCCCC ATTTT TAGGC AAAATCATAT ACAGACTATC CCAATATTGC CAGAGCTTTG	1860
ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAATGG ACTCCCAGTT GGAATAAATT	1920
TTTAGTCTCC CCCGGCGCTG GAGTTTTTTT GTAGTTAATG GCGGTATAAT GTGAAAGTTT	1980
TTTATCTATT TAAATTTATA A ATG CTA ACA GCG GAA AGA ATT AAA TTT ACC	2031
Met Leu Thr Ala Glu Arg Ile Lys Phe Thr	10
1 5	
CAG AAA CGG GGG TTT CGT CGG GTA CTA AAC CAA CGG GTG GAT GCC TAC	2079
Gln Lys Arg Gly Phe Arg Arg Val Leu Asn Gln Arg Val Asp Ala Tyr	25
15 20	

TTT	GCC	GAG	CAT	GGC	CTG	ACC	CAA	AGG	GAT	AAT	CCC	TCC	ATG	TAT	CTG	2127
Phe	Ala	Glu	His	Gly	Leu	Thr	Gln	Arg	Asp	Asn	Pro	Ser	Met	Tyr	Leu	
			30					35					40			
AAA	ACC	CTG	ATT	ATT	GTG	CTC	TGG	TTG	TTT	TCC	GCT	TGG	GCC	TTT	GTG	2175
Lys	Thr	Leu	Ile	Ile	Val	Leu	Trp	Leu	Phe	Ser	Ala	Trp	Ala	Phe	Val	
		45					50					55				
CTT	TTT	GCT	CCA	GTT	ATT	TTT	CCG	GTG	CGC	CTA	CTG	GGT	TGT	ATG	GTT	2223
Leu	Phe	Ala	Pro	Val	Ile	Phe	Pro	Val	Arg	Leu	Leu	Gly	Cys	Met	Val	
	60					65					70					
TTG	GCG	ATC	GCC	TTG	GCG	GCC	TTT	TCC	TTC	AAT	GTC	GGC	CAC	GAT	GCC	2271
Leu	Ala	Ile	Ala	Leu	Ala	Ala	Phe	Ser	Phe	Asn	Val	Gly	His	Asp	Ala	
	75				80					85					90	
AAC	CAC	AAT	GCC	TAT	TCC	TCC	AAT	CCC	CAC	ATC	AAC	CGG	GTT	CTG	GGC	2319
Asn	His	Asn	Ala	Tyr	Ser	Ser	Asn	Pro	His	Ile	Asn	Arg	Val	Leu	Gly	
				95					100					105		
ATG	ACC	TAC	GAT	TTT	GTC	GGG	TTA	TCT	AGT	TTT	CTT	TGG	CGC	TAT	CGC	2367
Met	Thr	Tyr	Asp	Phe	Val	Gly	Leu	Ser	Ser	Phe	Leu	Trp	Arg	Tyr	Arg	
			110					115					120			
CAC	AAC	TAT	TTG	CAC	CAC	ACC	TAC	ACC	AAT	ATT	CTT	GGC	CAT	GAC	GTG	2415
His	Asn	Tyr	Leu	His	His	Thr	Tyr	Thr	Asn	Ile	Leu	Gly	His	Asp	Val	
		125					130					135				
GAA	ATC	CAT	GGA	GAT	GGC	GCA	GTA	CGT	ATG	AGT	CCT	GAA	CAA	GAA	CAT	2463
Glu	Ile	His	Gly	Asp	Gly	Ala	Val	Arg	Met	Ser	Pro	Glu	Gln	Glu	His	
	140					145					150					
GTT	GGT	ATT	TAT	CGT	TTC	CAG	CAA	TTT	TAT	ATT	TGG	GGT	TTA	TAT	CTT	2511
Val	Gly	Ile	Tyr	Arg	Phe	Gln	Gln	Phe	Tyr	Ile	Trp	Gly	Leu	Tyr	Leu	
	155				160					165					170	
TTC	ATT	CCC	TTT	TAT	TGG	TTT	CTC	TAC	GAT	GTC	TAC	CTA	GTG	CTT	AAT	2559
Phe	Ile	Pro	Phe	Tyr	Trp	Phe	Leu	Tyr	Asp	Val	Tyr	Leu	Val	Leu	Asn	
				175					180					185		
AAA	GGC	AAA	TAT	CAC	GAC	CAT	AAA	ATT	CCT	CCT	TTC	CAG	CCC	CTA	GAA	2607
Lys	Gly	Lys	Tyr	His	Asp	His	Lys	Ile	Pro	Pro	Phe	Gln	Pro	Leu	Glu	
			190					195					200			
TTA	GCT	AGT	TTG	CTA	GGG	ATT	AAG	CTA	TTA	TGG	CTC	GGC	TAC	GTT	TTC	2655
Leu	Ala	Ser	Leu	Leu	Gly	Ile	Lys	Leu	Leu	Trp	Leu	Gly	Tyr	Val	Phe	
		205					210					215				
GGC	TTA	CCT	CTG	GCT	CTG	GGC	TTT	TCC	ATT	CCT	GAA	GTA	TTA	ATT	GGT	2703
Gly	Leu	Pro	Leu	Ala	Leu	Gly	Phe	Ser	Ile	Pro	Glu	Val	Leu	Ile	Gly	
	220					225					230					
GCT	TCG	GTA	ACC	TAT	ATG	ACC	TAT	GGC	ATC	GTG	GTT	TGC	ACC	ATC	TTT	2751
Ala	Ser	Val	Thr	Tyr	Met	Thr	Tyr	Gly	Ile	Val	Val	Cys	Thr	Ile	Phe	
	235				240					245					250	

ATG	CTG	GCC	CAT	GTG	TTG	GAA	TCA	ACT	GAA	TTT	CTC	ACC	CCC	GAT	GGT	2799
Met	Leu	Ala	His	Val	Leu	Glu	Ser	Thr	Glu	Phe	Leu	Thr	Pro	Asp	Gly	
				255					260					265		
GAA	TCC	GGT	GCC	ATT	GAT	GAC	GAG	TGG	GCT	ATT	TGC	CAA	ATT	CGT	ACC	2847
Glu	Ser	Gly	Ala	Ile	Asp	Asp	Glu	Trp	Ala	Ile	Cys	Gln	Ile	Arg	Thr	
			270					275					280			
ACG	GCC	AAT	TTT	GCC	ACC	AAT	AAT	CCC	TTT	TGG	AAC	TGG	TTT	TGT	GGC	2895
Thr	Ala	Asn	Phe	Ala	Thr	Asn	Asn	Pro	Phe	Trp	Asn	Trp	Phe	Cys	Gly	
		285					290					295				
GGT	TTA	AAT	CAC	CAA	GTT	ACC	CAC	CAT	CTT	TTC	CCC	AAT	ATT	TGT	CAT	2943
Gly	Leu	Asn	His	Gln	Val	Thr	His	His	Leu	Phe	Pro	Asn	Ile	Cys	His	
	300					305					310					
ATT	CAC	TAT	CCC	CAA	TTG	GAA	AAT	ATT	ATT	AAG	GAT	GTT	TGC	CAA	GAG	2991
Ile	His	Tyr	Pro	Gln	Leu	Glu	Asn	Ile	Ile	Lys	Asp	Val	Cys	Gln	Glu	
315				320						325					330	
TTT	GGT	GTG	GAA	TAT	AAA	GTT	TAT	CCC	ACC	TTC	AAA	GCG	GCG	ATC	GCC	3039
Phe	Gly	Val	Glu	Tyr	Lys	Val	Tyr	Pro	Thr	Phe	Lys	Ala	Ala	Ile	Ala	
			335						340					345		
TCT	AAC	TAT	CGC	TGG	CTA	GAG	GCC	ATG	GGC	AAA	GCA	TCG	TGACATTGCC			3088
Ser	Asn	Tyr	Arg	Trp	Leu	Glu	Ala	Met	Gly	Lys	Ala	Ser				
			350					355					360			
TTGGGATTGA	AGCAAAATGG	CAAAATCCCT	CGTAAATCTA	TGATCGAAGC	CTTTCTGTG											3148
CCGCCGACC	AAATCCCCGA	TGCTGACCAA	AGGTTGATGT	TGGCATTGCT	CCAAACCCAC											3208
TTTGAGGGGG	TTCATTGGCC	GCAGTTTCAA	GCTGACCTAG	GAGGCAAAGA	TTGGGTGATT											3268
TTGCTCAAAT	CCGCTGGGAT	ATTGAAAGGC	TTCACCACCT	TTGGTTTCTA	CCCTGCTCAA											3328
TGGGAAGGAC	AAACCGTCAG	AATTGTTTAT	TCTGGTGACA	CCATCACCGA	CCCATCCATG											3388
TGGTCTAACC	CAGCCCTGGC	CAAGGCTTGG	ACCAAGGCCA	TGCAAATTCT	CCACGAGGCT											3448
AGGCCAGAAA	AATTATATTG	GCTCCTGATT	TCTTCCGGCT	ATCGCACCTA	CCGATTTTTG											3508
AGCATTTTTG	CCAAGGAATT	CTATCCCCAC	TATCTCCATC	CCACTCCCCC	GCCTGTACAA											3568
AATTTTATCC	ATCAGCTAGC															3588

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

58

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Leu	Thr	Ala	Glu	Arg	Ile	Lys	Phe	Thr	Gln	Lys	Arg	Gly	Phe	Arg	1	5	10	15
Arg	Val	Leu	Asn	Gln	Arg	Val	Asp	Ala	Tyr	Phe	Ala	Glu	His	Gly	Leu	20	25	30	
Thr	Gln	Arg	Asp	Asn	Pro	Ser	Met	Tyr	Leu	Lys	Thr	Leu	Ile	Ile	Val	35	40	45	
Leu	Trp	Leu	Phe	Ser	Ala	Trp	Ala	Phe	Val	Leu	Phe	Ala	Pro	Val	Ile	50	55	60	
Phe	Pro	Val	Arg	Leu	Leu	Gly	Cys	Met	Val	Leu	Ala	Ile	Ala	Leu	Ala	65	70	75	
Ala	Phe	Ser	Phe	Asn	Val	Gly	His	Asp	Ala	Asn	His	Asn	Ala	Tyr	Ser	85	90	95	
Ser	Asn	Pro	His	Ile	Asn	Arg	Val	Leu	Gly	Met	Thr	Tyr	Asp	Phe	Val	100	105	110	
Gly	Leu	Ser	Ser	Phe	Leu	Trp	Arg	Tyr	Arg	His	Asn	Tyr	Leu	His	His	115	120	125	
Thr	Tyr	Thr	Asn	Ile	Leu	Gly	His	Asp	Val	Glu	Ile	His	Gly	Asp	Gly	130	135	140	
Ala	Val	Arg	Met	Ser	Pro	Glu	Gln	Glu	His	Val	Gly	Ile	Tyr	Arg	Phe	145	150	155	
Gln	Gln	Phe	Tyr	Ile	Trp	Gly	Leu	Tyr	Leu	Phe	Ile	Pro	Phe	Tyr	Trp	165	170	175	
Phe	Leu	Tyr	Asp	Val	Tyr	Leu	Val	Leu	Asn	Lys	Gly	Lys	Tyr	His	Asp	180	185	190	
His	Lys	Ile	Pro	Pro	Phe	Gln	Pro	Leu	Glu	Leu	Ala	Ser	Leu	Leu	Gly	195	200	205	
Ile	Lys	Leu	Leu	Trp	Leu	Gly	Tyr	Val	Phe	Gly	Leu	Pro	Leu	Ala	Leu	210	215	220	
Gly	Phe	Ser	Ile	Pro	Glu	Val	Leu	Ile	Gly	Ala	Ser	Val	Thr	Tyr	Met	225	230	235	
Thr	Tyr	Gly	Ile	Val	Val	Cys	Thr	Ile	Phe	Met	Leu	Ala	His	Val	Leu	245	250	255	
Glu	Ser	Thr	Glu	Phe	Leu	Thr	Pro	Asp	Gly	Glu	Ser	Gly	Ala	Ile	Asp	260	265	270	

Asp Glu Trp Ala Ile Cys Gln Ile Arg Thr Thr Ala Asn Phe Ala Thr
275 280 285

Asn Asn Pro Phe Trp Asn Trp Phe Cys Gly Gly Leu Asn His Gln Val
290 295 300

Thr His His Leu Phe Pro Asn Ile Cys His Ile His Tyr Pro Gln Leu
305 310 315 320

Glu Asn Ile Ile Lys Asp Val Cys Gln Glu Phe Gly Val Glu Tyr Lys
325 330 335

Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala Ser Asn Tyr Arg Trp Leu
340 345 350

Glu Ala Met Gly Lys Ala Ser
355

0034254-09159
155750-45242699

2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1884 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCTTCACTT CGGTTTTATA TTGTGACCAT GGTTCACAGG CATCTGCTCT AGGGAGTTTT	60
TCCGCTGCCT TTAGAGAGTA TTTTCTCCAA GTCGGCTAAC TCCCCCATTT TTAGGCAAAA	120
TCATATACAG ACTATCCCAA TATTGCCAGA GCTTTGATGA CTCACTGTAG AAGGCAGACT	180
AAAATTCTAG CAATGGACTC CCAGTTGGAA TAAATTTTTTA GTCTCCCCCG GCGCTGGAGT	240
TTTTTTGTAG TTAATGGCGG TATAATGTGA AAGTTTTTTTA TCTATTTAAA TTTATAAATG	300
CTAACAGCGG AAAGAATTAA ATTTACCCAG AAACGGGGGT TTCGTCGGGT ACTAAACCAA	360
CGGGTGGATG CCTACTTTGC CGAGCATGGC CTGACCCAAA GGGATAATCC CTCCATGTAT	420
CTGAAAACCC TGATTATTGT GCTCTGGTTG TTTTCCGCTT GGGCCTTTGT GCTTTTTGCT	480
CCAGTTATTT TTCCGGTGCG CCTACTGGGT TGTATGGTTT TGGCGATCGC CTTGGCGGCC	540
TTTTCCTTCA ATGTCGGCCA CGATGCCAAC CACAATGCCT ATTCCTCCAA TCCCCACATC	600
AACCGGGTTC TGGGCATGAC CTACGATTTT GTCGGGTTAT CTAGTTTTCT TTGGCGCTAT	660
CGCCACAAC TTTTGCACCA CACCTACACC AATATTCTTG GCCATGACGT GGAAATCCAT	720

GGAGATGGCG	CAGTACGTAT	GAGTCCTGAA	CAAGAACATG	TTGGTATTTA	TCGTTTCCAG	780
CAATTTTATA	TTTGGGGTTT	ATATCTTTTC	ATTCCCTTTT	ATTGGTTTCT	CTACGATGTC	840
TACCTAGTGC	TTAATAAAGG	CAAATATCAC	GACCATAAAA	TTCTCCTTTT	CCAGCCCCTA	900
GAATTAGCTA	GTTTGCTAGG	GATTAAGCTA	TTATGGCTCG	GCTACGTTTT	CGGCTTACCT	960
CTGGCTCTGG	GCTTTTCCAT	TCCTGAAGTA	TTAATTGGTG	CTTCGGTAAC	CTATATGACC	1020
TATGGCATCG	TGGTTTGCAC	CATCTTTATG	CTGGCCCATG	TGTTGGAATC	AACTGAATTT	1080
CTCACCCCCG	ATGGTGAATC	CGGTGCCATT	GATGACGAGT	GGGCTATTTG	CCAAATTCGT	1140
ACCACGGCCA	ATTTTGCCAC	CAATAATCCC	TTTTGGAACT	GGTTTTGTGG	CGGTTTAAAT	1200
CACCAAGTTA	CCCACCATCT	TTTCCCCAAT	ATTTGTCATA	TTCACTATCC	CCAATTGGAA	1260
AATATTATTA	AGGATGTTTG	CCAAGAGTTT	GGTGTGGAAT	ATAAAGTTTA	TCCCACCTTC	1320
AAAGCGGCGA	TCGCCTCTAA	CTATCGCTGG	CTAGAGGCCA	TGGGCAAAGC	ATCGTGACAT	1380
TGCCTTGGA	TTGAAGCAAA	ATGGCAAAAT	CCCTCGTAAA	TCTATGATCG	AAGCCTTTCT	1440
GTTGCCCCGCC	GACCAAATCC	CCGATGCTGA	CCAAAGGTTG	ATGTTGGCAT	TGCTCCAAAC	1500
CCACTTTGAG	GGGGTTCATT	GGCCGCAGTT	TCAAGCTGAC	CTAGGAGGCA	AAGATTGGGT	1560
GATTTTGCTC	AAATCCGCTG	GGATATTGAA	AGGCTTCACC	ACCTTTGGTT	TCTACCCTGC	1620
TCAATGGGAA	GGACAAACCG	TCAGAATTGT	TTATTCTGGT	GACACCATCA	CCGACCCATC	1680
CATGTGGTCT	AACCCAGCCC	TGGCCAAGGC	TTGGACCAAG	GCCATGCAAA	TTCTCCACGA	1740
GGCTAGGCCA	GAAAAATTAT	ATTGGCTCCT	GATTTCTTCC	GGCTATCGCA	CCTACCGATT	1800
TTTGAGCATT	TTTGCCAAGG	AATTCTATCC	CCACTATCTC	CATCCCCTC	CCCCGCCTGT	1860
ACAAAATTTT	ATCCATCAGC	TAGC				1884

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1685 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATATCTGCC TACCCTCCCA AAGAGAGTAG TCATTTTTC TCAATGGCTG CTCAAATCAA

61

GAAATACATT	ACCTCAGATG	AACTCAAGAA	CCACGATAAA	CCCGGAGATC	TATGGATCTC	120
GATTCAAGGG	AAAGCCTATG	ATGTTTCGGA	TTGGGTGAAA	GACCATCCAG	GTGGCAGCTT	180
TCCCTTGAAG	AGTCTTGCTG	GTCAAGAGGT	AACTGATGCA	TTTGTTGCAT	TCCATCCTGC	240
CTCTACATGG	AAGAATCTTG	ATAAGTTTTT	CACTGGGTAT	TATCTTAAAG	ATTACTCTGT	300
TTCTGAGGTT	TCTAAAGATT	ATAGGAAGCT	TGTGTTTGAG	TTTTCTAAAA	TGGGTTTGTA	360
TGACAAAAAA	GGTCATATTA	TGTTTGCAAC	TTTGTGCTTT	ATAGCAATGC	TGTTTGCTAT	420
GAGTGTTTAT	GGGGTTTTGT	TTTGTGAGGG	TGTTTTGGTA	CATTTGTTTT	CTGGGTGTTT	480
GATGGGGTTT	CTTTGGATTC	AGAGTG GTTG	GATTGGACAT	GATGCTGGGC	ATTATATGGT	540
AGTGTCTGAT	TCAAGGCTTA	ATAAGTTTAT	GGGTATTTTT	GCTGCAAATT	GTCTTTCAGG	600
AATAAGTATT	GGTTGGTGGA	AATGGAACCA	TAATGCACAT	CACATTGCCT	GTAATAGCCT	660
TGAATATGAC	CCTGATTTAC	AATATATACC	ATTCCTTGTT	GTGTCTTCCA	AGTTTTTTGG	720
PTCACTCACC	TCTCATTTCT	ATGAGAAAAG	GTTGACTTTT	GACTCTTTAT	CAAGATTCTT	780
TGTAAGTTAT	CAACATTGGA	CATTTTACCC	TATTATGTGT	GCTGCTAGGC	TCAATATGTA	840
TGTACAATCT	CTCATAATGT	TGTTGACCAA	GAGAAATGTG	TCCTATCGAG	CTCAGGAACT	900
ETTGGGATGC	CTAGTGTTCT	CGATTTGGTA	CCCGTTGCTT	GTTTCTTGTT	TGCCTAATTG	960
GGGTGAAAGA	ATTATGTTTG	TTATTGCAAG	TTTATCAGTG	ACTGGAATGC	AACAAGTTCA	1020
GTTCTCCTTG	AACCACTTCT	CTTCAAGTGT	TTATGTTGGA	AAGCCTAAAG	GGAATAATTG	1080
GTTTGAGAAA	CAAACGGATG	GGACACTTGA	CATTTCTTGT	CCTCCTTGGA	TGGATTGGTT	1140
TCATGGTGGA	TTGCAATTCC	AAATTGAGCA	TCATTTGTTT	CCCAAGATGC	CTAGATGCAA	1200
CCTTAGGAAA	ATCTCGCCCT	ACGTGATCGA	GTTATGCAAG	AAACATAATT	TGCCTTACAA	1260
TTATGCATCT	TTCTCCAAGG	CCAATGAAAT	GACACTCAGA	ACATTGAGGA	ACACAGCATT	1320
GCAGGCTAGG	GATATAACCA	AGCCGCTCCC	GAAGAATTTG	GTATGGGAAG	CTCTTCACAC	1380
TCATGGTTAA	AATTACCCTT	AGTTCATGTA	ATAATTTGAG	ATTATGTATC	TCCTATGTTT	1440
GTGTCTTGTC	TTGGTTCTAC	TTGTTGGAGT	CATTGCAACT	TGTCTTTTAT	GGTTTATTAG	1500
ATGTTTTTTA	ATATATTTTA	GAGGTTTTGC	TTTCATCTCC	ATTATTGATG	AATAAGGAGT	1560
TGCATATTGT	CAATTGTTGT	GCTCAATATC	TGATATTTTG	GAATGTACTT	TGTACCACTG	1620
TGTTTTTCAGT	TGAAGCTCAT	GTGTACTTCT	ATAGACTTTG	TTTAAATGGT	TATGTCATGT	1680
TATTT						1685

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ala Ala Gln Ile Lys Lys Tyr Ile Thr Ser Asp Glu Leu Lys Asn
1          5          10
His Asp Lys Pro Gly Asp Leu Trp Ile Ser Ile Gln Gly Lys Ala Tyr
20          25          30
Asp Val Ser Asp Trp Val Lys Asp His Pro Gly Gly Ser Phe Pro Leu
35          40          45
Lys Ser Leu Ala Gly Gln Glu Val Thr Asp Ala Phe Val Ala Phe His
50          55          60
Pro Ala Ser Thr Trp Lys Asn Leu Asp Lys Phe Phe Thr Gly Tyr Tyr
65          70          75          80
Leu Lys Asp Tyr Ser Val Ser Glu Val Ser Lys Asp Tyr Arg Lys Leu
85          90          95
Val Phe Glu Phe Ser Lys Met Gly Leu Tyr Asp Lys Lys Gly His Ile
100          105          110
Met Phe Ala Thr Leu Cys Phe Ile Ala Met Leu Phe Ala Met Ser Val
115          120          125
Tyr Gly Val Leu Phe Cys Glu Gly Val Leu Val His Leu Phe Ser Gly
130          135          140
Cys Leu Met Gly Phe Leu Trp Ile Gln Ser Gly Trp Ile Gly His Asp
145          150          155          160
Ala Gly His Tyr Met Val Val Ser Asp Ser Arg Leu Asn Lys Phe Met
165          170          175
Gly Ile Phe Ala Ala Asn Cys Leu Ser Gly Ile Ser Ile Gly Trp Trp
180          185          190
Lys Trp Asn His Asn Ala His His Ile Ala Cys Asn Ser Leu Glu Tyr
195          200          205
Asp Pro Asp Leu Gln Tyr Ile Pro Phe Leu Val Val Ser Ser Lys Phe
210          215          220

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Phe Gly Ser Leu Thr Ser His Phe Tyr Glu Lys Arg Leu Thr Phe Asp
 225 230 235 240
 Ser Leu Ser Arg Phe Phe Val Ser Tyr Gln His Trp Thr Phe Tyr Pro
 245 250 255
 Ile Met Cys Ala Ala Arg Leu Asn Met Tyr Val Gln Ser Leu Ile Met
 260 265 270
 Leu Leu Thr Lys Arg Asn Val Ser Tyr Arg Ala Gln Glu Leu Leu Gly
 275 280 285
 Cys Leu Val Phe Ser Ile Trp Tyr Pro Leu Leu Val Ser Cys Leu Pro
 290 295 300
 Asn Trp Gly Glu Arg Ile Met Phe Val Ile Ala Ser Leu Ser Val Thr
 305 310 315 320
 Gly Met Gln Gln Val Gln Phe Ser Leu Asn His Phe Ser Ser Ser Val
 325 330 335
 Tyr Val Gly Lys Pro Lys Gly Asn Asn Trp Phe Glu Lys Gln Thr Asp
 340 345 350
 Gly Thr Leu Asp Ile Ser Cys Pro Pro Trp Met Asp Trp Phe His Gly
 355 360 365
 Gly Ser Gln Phe Gln Ile Glu His His Leu Phe Pro Lys Met Pro Arg
 370 375 380
 Cys Asn Leu Arg Lys Ile Ser Pro Tyr Val Ile Glu Leu Cys Lys Lys
 385 390 395 400
 His Asn Leu Pro Tyr Asn Tyr Ala Ser Phe Ser Lys Ala Asn Glu Met
 405 410 415
 Thr Leu Arg Thr Leu Arg Asn Thr Ala Leu Gln Ala Arg Asp Ile Thr
 420 425 430
 Lys Pro Leu Pro Lys Asn Leu Val Trp Glu Ala Leu His Thr His Gly
 435 440 445

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

64

Trp Ile Gly His Asp Ala Gly His
1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Val Gly His Asp Ala Asn His
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Val Leu Gly His Asp Cys Gly His
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (peptide)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Ile Ala His Glu Cys Gly His
1 5

65